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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=9; day=23; hr=12; min=55; sec=41; ms=731;]

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Application No: 10585149 Version No: 2.0

Input Set:

Output Set:

Started: 2008-08-25 13:32:03.562
Finished: 2008-08-25 13:32:06.481
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 919 ms
Total Warnings: 36
Total Errors: 0
No. of SeqIDs Defined: 56
Actual SeqID Count: 56

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (20)
W 402	Undefined organism found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)

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Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> BEBBINGTON, CHRISTOPHER ROBERT
YU, BO

<120> TRANSACTIVATION SYSTEM FOR MAMMALIAN CELLS

<130> 73678-026

<140> 10585149
<141> 2008-08-25

<150> PCT/US2004/043830
<151> 2004-12-30

<150> 60/533,917
<151> 2003-12-13

<160> 56

<170> PatentIn version 3.5

<210> 1
<211> 236
<212> PRT
<213> Cricetulus longicaudatus

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1 5 10 15

Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Val
20 25 30

Gly Asp Val Asp Ala Ala Pro Leu Gly Ala Ala Pro Thr Pro Gly Ile
35 40 45

Phe Ser Phe Gln Pro Glu Ser Asn Pro Thr Pro Ala Val His Arg Asp
50 55 60

Met Ala Ala Arg Thr Ser Pro Leu Arg Pro Ile Val Ala Thr Thr Gly
65 70 75 80

Pro Thr Leu Ser Pro Val Pro Val Val His Leu Thr Leu Arg Arg
85 90 95

Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Arg Asp Phe Ala Glu Met
100 105 110

Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly Arg Phe Ala
115 120 125

Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile
130 135 140

Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu Ser Val Asn
145 150 155 160

Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp Met Thr Glu
165 170 175

Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn Gly Gly Trp
180 185 190

Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Val Arg Pro Leu Phe Asp
195 200 205

Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala Leu Val Gly
210 215 220

Ala Cys Ile Thr Leu Gly Thr Tyr Leu Gly His Lys
225 230 235

<210> 2
<211> 195
<212> PRT
<213> Cricetulus longicaudatus

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Met Ala Gln Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
1 5 10 15

Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Val
20 25 30

Gly Asp Val Asp Ala Ala Ala Ala Ala Ser Pro Val Pro Pro Val
35 40 45

Val His Leu Thr Leu Arg Arg Ala Gly Asp Asp Phe Ser Arg Arg Tyr
50 55 60

Arg Arg Asp Phe Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe
65 70 75 80

Thr Ala Arg Gly Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp
85 90 95

Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val
100 105 110

Met Cys Val Glu Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn
115 120 125

Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp
130 135 140

Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro
145 150 155 160

Ser Val Arg Pro Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu
165 170 175

Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Thr Tyr Leu
180 185 190

Gly His Lys
195

<210> 3

<211> 588

<212> DNA

<213> Cricetulus longicaudatus

<400> 3

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tataagctgt cacagagggg ctacgagtgg gatgtggag atgtggacgc cgccggcccg 120

gccgcgagcc ccgtgccacc tgtggtccac ctgaccctcc gccgggctgg ggatgacttc 180

tcccgtcgct accgtcgcga cttcgccggag atgtccagtc agctgcaccc tgcgccttc 240

accgcgaggg gacgcgttgc tacgggtggg gaggaactct tcagggatgg ggtgaactgg 300

gggaggattg tggccttctt tgagttcggt ggggtcatgt gtgtggagag cgtcaacagg 360

gagatgtcac ccctggtgga caacatcgcc ctgtggatga ccgagtacct gaaccggcat 420

ctgcacacacct ggatccagga taacggaggc tgggacgcatttggactgtacggcccc 480

agtgtgaggc ctctgtttga ttctcttgg ctgtctctga agaccctgct cagcctggcc 540

ctggtcgggg cctgcac tacgttacc tacctggcc acaagtga 588

<210> 4

<211> 289

<212> PRT

<213> Human adenovirus type 5

<400> 4

Met Arg His Ile Ile Cys His Gly Gly Val Ile Thr Glu Glu Met Ala
1 5 10 15

Ala Ser Leu Leu Asp Gln Leu Ile Glu Glu Val Leu Ala Asp Asn Leu
20 25 30

Pro Pro Pro Ser His Phe Glu Pro Pro Thr Leu His Glu Leu His Asp
35 40 45

Leu Asp Val Thr Ala Pro Glu Asp Pro Asn Glu Glu Ala Val Ser Gln
50 55 60

Ile Phe Pro Asp Ser Val Met Leu Ala Val Gln Glu Gly Ile Asp Leu
65 70 75 80

Leu Thr Phe Pro Pro Ala Pro Gly Ser Pro Glu Pro Pro His Leu Ser
85 90 95

Arg Gln Pro Glu Gln Pro Glu Gln Arg Ala Leu Gly Pro Val Ser Met
100 105 110

Pro Asn Leu Val Pro Glu Val Ile Asp Leu Thr Gly His Glu Ala Gly
115 120 125

Phe Pro Pro Ser Asp Asp Glu Asp Glu Glu Gly Glu Glu Phe Val Leu
130 135 140

Asp Tyr Val Glu His Pro Gly His Gly Cys Arg Ser Cys His Tyr His
145 150 155 160

Arg Arg Asn Thr Gly Asp Pro Asp Ile Met Cys Ser Leu Cys Tyr Met
165 170 175

Arg Thr Cys Gly Met Phe Val Tyr Ser Pro Val Ser Glu Pro Glu Pro
180 185 190

Glu Pro Glu Pro Glu Pro Ala Arg Pro Thr Arg Arg Pro Lys
195 200 205

Met Ala Pro Ala Ile Leu Arg Arg Pro Thr Ser Pro Val Ser Arg Glu
210 215 220

Cys Asn Ser Ser Thr Asp Ser Cys Asp Ser Gly Pro Ser Asn Thr Pro
225 230 235 240

Pro Glu Ile His Pro Val Val Pro Leu Cys Pro Ile Lys Pro Val Ala
245 250 255

Val Arg Val Gly Gly Arg Arg Gln Ala Val Glu Cys Ile Glu Asp Leu
260 265 270

Leu Asn Glu Pro Gly Gln Pro Leu Asp Leu Ser Cys Lys Arg Pro Arg
275 280 285

Pro

<210> 5
<211> 986
<212> DNA
<213> Human adenovirus type 5

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gaccagctga tcgaagaggt actggctgat a atcttccac ctcc tagcca ttttgaacca 120
cctacccttc acgaactgca tgatttagac gtgacggccc ccgaagatcc caacgaggag 180
gcggtttgc agattttcc cgactctgta atgttggcg tgcaggaagg gattgactta 240
ctcactttc cggccggcc cggttctccg gagccgcctc accttcccg gcagccccag 300
cagccggagc agagagcctt gggtccgggt tctatgccaa accttgtacc ggaggtgatc 360
gatcttaccg gccacgaggc tggcttcca cccagtgacg acgaggatga agagggtgag 420
gagtttgt tagattatgt ggagcacccc gggcacgggtt gcaggtcttgc tcattatcac 480
cgaggaaata cgggggaccc agatattatg tggcgctt gctatatgag gacctgtggc 540
atgtttgtct acagtaagtg aaaattatgg gcagtgggtg atagagtggt gggtttggtg 600
tggtaatttt tttttaatt tttacagttt tgggtttaa agaattttgtt attgtgattt 660
ttttaaaagg tcctgtgtct gaacctgagc ctgagcccgaa gccagaaccg gagcctgcaa 720

gacctacccg ccgtcctaaa atggcgccctg ctatcctgag acgcccgaca tcacctgtgt 780
ctagagaatg caatagtagt acggatagct gtgactccgg tccttctaac acacctcctg 840
agatacaccc ggtggtcccg ctgtgccccca ttaaaccagt tgccgtgaga gttggtgggc 900
gtcgccaggc tgtggaatgt atcgaggact tgcttaacga gcctgggcaa cctttggact 960
tgagctgtaa acgccccagg ccataa 986

<210> 6
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 6
cccgaaattcg ccgccaccat gagacatatt atctgccac 39

<210> 7
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 7
cccggtcgacc ttatggcctg gggcgttt 28

<210> 8
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 8
cccggttaccg ccgccaccat gagacatatt atctgccac 39

<210> 9
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 9

cccgccggccg ccttatggcc tggggcggtt

30

<210> 10

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 10

ggaggtgatc gatcttaccg gccac

25

<210> 11

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 11

cctacccttc acgaactgca tgatttagac gtgacg

36

<210> 12

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 12

cgtcacgtct aaatcatgca gttcgtgaag ggtagg

36

<210> 13

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 13

cccgaaattcg ccgccaccat ggaggcttgg gagtgttt

38

<210> 14
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 14
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<210> 15
 <211> 558
 <212> DNA
 <213> Human adenovirus type 5

<400> 15
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 ttgttggaaac agagctctaa cagtagcttct tggtttggaa gtttctgtg gggctcatcc 120
 caggcaaaat tagtctgcag aattaaggag gattacaatgt gggaaatttga agagctttg 180
 aaatcctgtg gtgagctgtt tgattctttt aatctgggtc accaggcgct tttccaagag 240
 aaggcatca agactttgga ttttccaca cggggggcgct ctgcggctgc tttttttttt 300
 ttgtttta taaaggataa atggagcgaa gaaaccatc tgacgggggg gtacctgtt 360
 gatttctgg ccatgcattt gtggagagcg gttgtgagac acaagaatcg cctgctactg 420
 ttgtcttccg tccgccccgc gataataccg acggaggagc agcagcagca gcaggaggaa 480
 gcccggccggc ggcggcagga gcagagccca tggaaaccgaa gagccggctt ggaccctcg 540
 gaatgaatgt tggtcgac 558

<210> 16
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 16
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<210> 17
 <211> 32

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 17
cccgccggccg ccggtcctga gatcctcatt tc

32

<210> 18
<211> 2824
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (16)..(2799)

<400> 18
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Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr
1 5 10

51

gcc gcc gct gcc gcg gaa ccc ccg gca ccg ccg ccg ccc cct
Ala Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro
15 20 25

99

cct gag gag gac cca gag cag gac agc ggc ccg gag gac ctg cct ctc
Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu
30 35 40

147

gtc agg ctt gag ttt gaa gaa aca gaa gaa cct gat ttt act gca tta
Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu
45 50 55 60

195

tgt cag aaa tta aag ata cca gat cat gtc aga gag aga gct tgg tta
Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu
65 70 75

243

act tgg gag aaa gtt tca tct gtg gat gga gta ttg gga ggt tat att
Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile
80 85 90

291

caa aag aaa aag gaa ctg tgg gga atc tgt atc ttt att gca cga gtt
Gln Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Arg Val
95 100 105

339

gac cta gat gag atg tcg ttc act tta ctg agc tac aga aaa aca tac
Asp Leu Asp Glu Met Ser Phe Thr Leu Leu Ser Tyr Arg Lys Thr Tyr
110 115 120

387

gaa atc agt gtc cat aaa ttc ttt aac tta cta aaa gaa att gat acc
Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr
125 130 135 140

435

agt acc aaa gtt gat aat gct atg tca aga ctg ttg aag aag tat gat Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp	145	150	155	483	
gta ttg ttt gca ctc ttc agc aaa ttg gaa agg aca tgt gaa ctt ata Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile	160	165	170	531	
tat ttg aca caa ccc agc agt tcg ata tct act gaa ata aat tct gca Tyr Leu Thr Gln Pro Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala	175	180	185	579	
ttg gtg cta aaa gtt tct tgg atc aca ttt tta tta gct aaa ggg gaa Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu	190	195	200	627	
gta tta caa atg gaa gat gat ctg gtg att tca ttt cag tta atg cta Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu	205	210	215	220	675
tgt gtc ctt gac tat ttt att aaa ctc tca cct ccc atg ttg ctc aaa Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys	225	230	235	723	
gaa cca tat aaa aca gct gtt ata ccc att aat ggt tca cct cga aca Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr	240	245	250	771	
ccc agg cga ggt cag aac agg agt gca cgg ata gca aaa caa cta gaa Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu	255	260	265	819	
aat gat aca aga att att gaa gtt ctc tgt aaa gaa cat gaa tgt aat Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn	270	275	280	867	
ata gat gag gtg aaa aat gtt tat ttc aaa aat ttt ata cct ttt atg Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met	285	290	295	300	915
aat tct ctt gga ctt gta aca tct aat gga ctt cca gag gtt gaa aat Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn	305	310	315	963	
ctt tct aaa cga tac gaa gaa att tat ctt aaa aat aaa gat cta gat Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp	320	325	330	1011	
cga aga tta ttt ttg gat cat gat aaa act ctt cag act gat tct ata Arg Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile	335	340	345	1059	
gac agt ttt gaa aca cag aga aca cca cga aaa agt aac ctt gat gaa Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu	350	355	360	1107	

gag gtg aat ata att cct cca cac act cca gtt agg act gtt atg aac 1155
Glu Val Asn Ile Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn
365 370 375 380

act atc caa caa tta atg att tta aat tct gca agt gat caa c